

## SEQUENCE LISTING

<110> Gao, Zeren  
 Hart, Charles E.  
 Piddington, Christopher S.  
 Sheppard, Paul O.  
 Shoemaker, Kimberly E.  
 Gilbertson, Debra G.  
 West, James W.

<120> GROWTH FACTOR HOMOLOG ZVEGF3

<130> 98-60C1

<160> 50

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<213> Homo sapiens

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cgccgtgagt gagctctcac ccagtcagc caa atg agc ctc ttc ggg ctt ctc	174
Met Ser Leu Phe Gly Leu Leu	
1 5	
ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa	222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu	
10 15 20	
tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac	270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn	
25 30 35	

143

009077" 99690760

T1430

gga gta caa gat cct cag cat gag aga att att act gtg tct act aat 318  
 Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn  
 40 45 50 55

gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg 366  
 Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr  
 60 65 70

gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414  
 Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln  
 75 80 85

ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462  
 Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile  
 90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata 510  
 Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile  
 105 110 115

tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct 558  
 Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser  
 120 125 130 135

aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct 606  
 Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro  
 140 145 150

tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc 654  
 Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe  
 155 160 165

aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg 702  
 Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu  
 170 175 180

gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt 750  
 Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu  
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09706969-110500

144

145

ctccaatcgt ggaaagaaaa ttaaagtgtg tattaaatag atcaccagct agtttcagag 1471  
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 ggtaatgtca gtacaggaaa aaaactgtgc aagtgagcac ctgattccgt tgccttgctt 1591  
 aactctaaag ctccatgtcc tgggcctaaa atcgtataaa atctggattt tttttttttt 1651  
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 20 25 30  
 Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg  
 35 40 45  
 Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro  
 50 55 60  
 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val  
 65 70 75 80  
 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu  
 85 90 95  
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu  
 100 105 110  
 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr  
 115 120 125  
 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe  
 130 135 140  
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr  
 145 150 155 160  
 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu  
 165 170 175  
 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala  
 180 185 190  
 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp  
 195 200 205  
 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly  
 210 215 220  
 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
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146

009706966-110600

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 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu  
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 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys  
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 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu  
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<222> (38)...(38)

<223> Xaa is any amino acid

<221> VARIANT

<222> (40)...(45)

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147

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<221> VARIANT  
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 Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 50 55 60  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
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<210> 4  
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148



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gtncargayc	cncarcayga	rmgnathath	acngtnwsna	cnaayggngws	nathcaywsn	180	
ccnmgnnttyc	cncayacnta	yccnmgnaay	acngtnytn	tntggmgnyt	ngtngcngtn	240	
gargaraayg	tntggathca	rytnacntty	gaygarmgt	tyggnytn	rgayccngar	300	
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mgnathmgnt	tygtngwsng	ygartaytty	ccnwsngarc	cnggnttytg	yathcaytay	480	
aayathgtna	tgccncartt	yacngargcn	gtngwsnccnw	sngtnytncc	nccnwsngcn	540	
ytncnytn	ayytnytnaa	yaaygcna	acngcnytn	snacnytn	rgayytnath	600	
mgntayytn	arccngarmg	ntggcarytn	gayytn	garg	ayytnaymg	nccnactgg	660
carytnytn	gnaargcntt	ygtnttygg	mgnaarwsnm	gngtngtn	yytnaayytn	720	
ytncngarg	argtnmgnyt	ntaywsntgy	acnccnmgna	aytywsngt	nwsnathmg	780	
gargarytna	armgnacnga	yacnathtty	tggccnggnt	gyytnytn	ngt	naarmngtgy	840
ggnggnaayt	gygcntgytg	yytncaaya	tgayaaygart	gycartgygt	nccnwsnaar	900	
gtncacnaara	artaycayga	rgtnytn	car	ytngmgnccna	aracnggngt	nmngnggnytn	960
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ggngwsnacng	gnggn					1035	

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150



<221> misc\_feature  
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17

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<210> 12

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<400> 12

avrcansng gnhhnan

17

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<220>

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<400> 13

caygargart gygaytg

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<223> Oligonucleotide primer

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<223> n = A,T,C or G

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17

<210> 18

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<212> DNA

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<211> 17

<212> DNA

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<400> 20

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<210> 21

<211> 17

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<210> 22

<211> 17

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<221> misc\_feature

<222> (1)...(17)

<400> 22

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<210> 23

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<223> Oligonucleotide primer

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<400> 23

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<211> 17

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cgtttgatga aagatttggg c 21

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<210> 28  
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<400> 28  
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<400> 29  
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18

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<400> 30  
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25

<210> 31  
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<400> 31  
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25

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27

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<223> Oligonucleotide primer

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<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC20.180

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35

<210> 35

<211> 32

<212> DNA

<213> Artificial Sequence

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32

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<212> DNA

<213> Homo sapiens

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<222> (226)...(1338)

<400> 36

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cagggcgagc gcaggcggcg agagcgcagg gcggcgcggc gtcggtcccg ggagcagaac 180  
ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc 237

Met His Arg Leu

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac 285  
 Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp  
 5 10 15 20

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc 333  
 Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala  
 25 30 35

aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga 381  
 Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg  
 40 45 50

gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga 429  
 Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg  
 55 60 65

ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac 477  
 Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His  
 70 75 80

tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga 525  
 Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly  
 85 90 95 100

tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt 573  
 Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val  
 105 110 115

gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga 621  
 Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly  
 120 125 130

cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa 669  
 His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys  
 135 140 145

atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag 717  
 Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys  
 150 155 160

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160

att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag 765  
 Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu  
 165 170 175 180

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac 813  
 Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn  
 185 190 195

tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa 861  
 Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys  
 200 205 210

aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat 909  
 Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn  
 215 220 225

cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct 957  
 Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro  
 230 235 240

cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg 1005  
 Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu  
 245 250 255 260

gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat 1053  
 Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn  
 265 270 275

tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc 1101  
 Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe  
 280 285 290

ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt 1149  
 Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys  
 295 300 305

gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg 1197  
 Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val  
 310 315 320

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg 1245  
 Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg  
 325 330 335 340

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161

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293  
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His  
                   345                               350                               355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338  
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg \*  
                   360                               365                               370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg agggtagat 1398  
 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458  
 agtggttgc gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518  
 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga ggttatatat 1578  
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 ttttggtata tataaccagg tacaccagag gttacatatg tttagagttag actcttaaaa 1698  
 tcctttgccaa aaataaggga tgggtcaaata tatgaaacat gtcttttagaa aatttaggag 1758  
 ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818  
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<210> 37

<211> 370

<212> PRT

<213> Homo sapiens

<400> 37

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys  
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 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala  
                   20                  25                  30  
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp  
                   35                  40                  45  
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val  
                   50                  55                  60  
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr  
   65                  70                  75                  80  
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp  
                   85                  90                  95  
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp  
                   100                  105                  110  
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly  
                   115                  120                  125

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Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr  
 130 135 140  
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys  
 145 150 155 160  
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala  
 165 170 175  
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly  
 180 185 190  
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp  
 195 200 205  
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu  
 210 215 220  
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr  
 225 230 235 240  
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser  
 245 250 255  
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys  
 260 265 270  
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala  
 275 280 285  
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly  
 290 295 300  
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser  
 305 310 315 320  
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly  
 325 330 335  
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
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163

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Met Leu Leu Leu Gly Leu Leu Leu  
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ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc 1120  
 Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser  
 10. 15 20

aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga 1168  
 Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly  
 25 30 35 40

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 Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly  
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agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg 1264  
 Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val  
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ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg 1312  
 Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu  
 75 80 85

aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc 1360  
 Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys  
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aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta 1408  
 Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu  
 105 110 115 120

gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa 1456  
 Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys  
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 Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser  
 140 145 150

gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca 1552  
 Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr  
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gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac 1600  
 Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp  
 170 175 180

ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att 1648  
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 Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys  
 220 225 230

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 Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr  
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agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag 1840  
 Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys  
 250 255 260

009071"89690260

166



agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888  
 Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys  
 265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936  
 Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys  
 285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984  
 Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg  
 300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032  
 Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala  
 315 320 325

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 330 335 340

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 Gly \*  
 345

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Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg  
35 40 45  
Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro  
50 55 60  
His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val  
65 70 75 80  
Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu  
85 90 95  
Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu  
100 105 110  
Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr  
115 120 125  
Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe  
130 135 140  
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr  
145 150 155 160  
Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu  
165 170 175  
Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala  
180 185 190  
Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp  
195 200 205  
Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly  
210 215 220  
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225 230 235 240

168

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169

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42

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170

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ccaagaaata	cggctcttgg	atggagatta	gtagcagtag	aggaaaatgt	atggatacaa	300
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